

GEPHE SUMMARY

	Gephebase Gene		GepheID
Proline specific permease PUT4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Proline specific permease PUT4" #gephebase-summary-title)		GP00001501	
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology" #gephebase-summary-title)			
	Trait		
Nitrogen use (growth rate on proline) (<a #gephebase-summary-title"="" (growth="" href="https://www.gephebase.org/search-criteria?/and+Trait=" nitrogen="" on="" proline)"="" rate="" use="">https://www.gephebase.org/search-criteria?/and+Trait="Nitrogen use (growth rate on proline)" #gephebase-summary-title)			
	Trait State in Taxon A		
Budding yeast			
	Trait State in Taxon B		
Budding yeast West African DBVPG6044 (WA)			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific" #gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Saccharomyces cerevisiae (<a #gephebase-summary-title"="" cerevisiae"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" saccharomyces="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces cerevisiae" #gephebase-summary-title)		Saccharomyces cerevisiae (<a #gephebase-summary-title"="" cerevisiae"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" saccharomyces="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces cerevisiae" #gephebase-summary-title)	
	Common Name		Common Name
baker's yeast		baker's yeast	
	Synonyms		Synonyms
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae		Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
	Parent		Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Budding yeast (wild strains - see article)		Budding yeast West African DBVPG6044 (WA)	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
PUT4		P15380 (http://www.uniprot.org/uniprot/P15380)	
	Synonyms		GenebankID or UniProtKB
YOR348C; O6345		M30583.1 (https://www.ncbi.nlm.nih.gov/nuccore/M30583.1)	
	String		
4932.YOR348C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YOR348C)			
	Sequence Similarities		
Belongs to the amino acid-polyamine-organocation (APC) superfamily. YAT (TC 2.A.3.10) family.			
	GO - Molecular Function		
GO:0015193 : L-proline transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015193)			
GO:0015175 : neutral amino acid transmembrane transporter activity			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015175>)

GO - Biological Process

GO:0015812 : gamma-aminobutyric acid transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015812>)

GO:0015804 : neutral amino acid transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015804>)

GO:0015824 : proline transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015824>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

Cis-regulatory ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Cis-regulatory+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=))

Aberration Type

Unknown ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=))

Molecular Details of the Mutation

several synonymous and promoter mutations

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Linkage Mapping+"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=))

Main Reference

Concerted evolution of life stage performances signals recent selection on yeast nitrogen use. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25349282>)

Authors

Ibstedt S; Stenberg S; BagÅ©s S; Gjuvland AB; Salinas F; Kourtchenko O; Samy JK; Blomberg A; Omholt SW; Liti G; Beltran G; Warringer J

Abstract

Exposing natural selection driving phenotypic and genotypic adaptive differentiation is an extraordinary challenge. Given that an organism's life stages are exposed to the same environmental variations, we reasoned that fitness components, such as the lag, rate, and efficiency of growth, directly reflecting performance in these life stages, should often be selected in concert. We therefore conjectured that correlations between fitness components over natural isolates, in a particular environmental context, would constitute a robust signal of recent selection. Critically, this test for selection requires fitness components to be determined by different genetic loci. To explore our conjecture, we exhaustively evaluated the lag, rate, and efficiency of asexual population growth of natural isolates of the model yeast *Saccharomyces cerevisiae* in a large variety of nitrogen-limited environments. Overall, fitness components were well correlated under nitrogen restriction. Yeast isolates were further crossed in all pairwise combinations and coinheritance of each fitness component and genetic markers were traced. Trait variations tended to map to quantitative trait loci (QTL) that were private to a single fitness component. We further traced QTLs down to single-nucleotide resolution and uncovered loss-of-function mutations in RIM15, PUT4, DAL1, and DAL4 as the genetic basis for nitrogen source use variations. Effects of SNPs were unique for a single fitness component, strongly arguing against pleiotropy between lag, rate, and efficiency of reproduction under nitrogen restriction. The strong correlations between life stage performances that cannot be explained by pleiotropy compellingly support adaptive differentiation of yeast nitrogen source use and suggest a generic approach for detecting selection.

Å© The Author 2014. Published by Oxford University Press on behalf of the Society for Molecular Biology and Evolution. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com.

Additional References

RELATED GEPHE

Related Genes

3 (Allantoin permease DAL4, Allantoinase DAL1, Serine/threonine protein kinase RIM15) ([https://www.gephebase.org/search-criteria?/or+Taxon ID="+4932+"/and+Trait=Nitrogen use/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

PUT4 encoding a high-affinity proline permease